ABSTRACT

A method for generating address/capture tags for use in a sensitive and rapid flow-cytometry based assay for the multiplexed analysis of SNPs based on polymerase-mediated primer extension using microspheres as solid supports is described. Single-nucleotide polymorphisms (SNPs) are the most abundant type of human genetic variation. These variable sites are present at high density in the genome, making them powerful tools for mapping and diagnosing disease-related alleles. Subnanomolar concentrations of sample in small volumes (10 ml) can be analyzed at rates greater than one sample per minute, without a wash step. Genomic analysis using multiplexing microsphere arrays, enables the simultaneous analysis of dozens, and potentially hundreds of SNPs per sample. The method has been tested by genotyping the Glu69 variant from the HLA DPB1 locus, a SNP associated with chronic beryllium disease, as well as HLA DPA1 alleles.